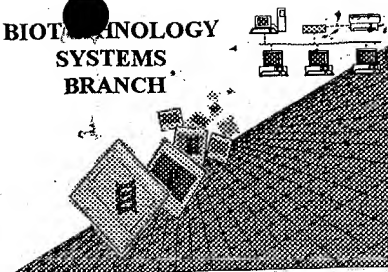# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/819,667A_

Source: _OIPE_

Date Processed by STIC: _7/31/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

```
       RAW SEQUENCE LISTING              DATE: 07/31/2001
       PATENT APPLICATION:   US/09/819,667A     TIME: 14:45:03

       Input Set : A:\#157155v1 -SEQUENCE LISTING ASCII.txt
       Output Set: N:\CRF3\07312001\I819667A.raw

    2 <110> APPLICANT: CANON INC.
    4 <120> TITLE OF INVENTION: Nucleic Acid Fragment Primer or Probe, and Method of
    5        Detecting Polyhydroxyalkanoate Synthesizing Microorganism by
    6        Using the Same
    8 <130> FILE REFERENCE: 4052014
   10 <140> CURRENT APPLICATION NUMBER: US/09/819,667A
   10 <141> CURRENT FILING DATE: 2001-03-29
   10 <160> NUMBER OF SEQ ID NOS: 9  18 (see below)
   12 <170> SOFTWARE: Microsoft Word
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
  100 <210> SEQ ID NO: 9
  101 <211> LENGTH: 30  25
  102 <212> TYPE: DNA
  103 <213> ORGANISM: Artificial Sequence
  105 <220> FEATURE:
  106 <223> OTHER INFORMATION: Primer for PCR multiplication
  108 <400> SEQUENCE: 9
E-> 109 ccaac agcgg bcayr tscag agcat    25
  199 <210> SEQ ID NO: 18
  200 <211> LENGTH: 30 25   last sequence in file
  201 <212> TYPE: DNA
  202 <213> ORGANISM: Artificial Sequence
  204 <220> FEATURE:
  205 <223> OTHER INFORMATION: Primer for PCR multiplication
  207 <400> SEQUENCE: 18
  208 ccaac agcgg gcatg tccag agcat    25
E-> 212 ny_maIn 157155 v 1
```

Per 1.822 of Sequence Rules, group all non-coding bases into groups of 10

→ group all bases into 10's (non-coding bases)

→ delete at end of file

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/819,667A

DATE: 07/31/2001
TIME: 14:45:04

Input Set : A:\#157155v1 -SEQUENCE LISTING ASCII.txt
Output Set: N:\CRF3\07312001\I819667A.raw

```
L:10  M:270 C: Current Application Number differs, Replaced Current Application No
L:10  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32  M:283 W: Missing Blank Line separator, <400> field identifier
L:109 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:25 SEQ:9
L:212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:212 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:33 SEQ:18
L:212 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:212 M:112 C: (48) String data converted to lower case,
L:212 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:33 SEQ:18
L:10  M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (9) Counted (18)
```